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Towards A Bioinformatics Platform For The Musa Research Community

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Current experiments in genomics produce a large amount of data that needs to be organized into databases and broadly accessible. Like other species, the Musa genomics community would benefit from centralized and innovative ways to study its genome. Over the past years, genetic and genomic data (e.g. BAC, EST, Markers) have been generated and stored in databases. Several pipelines of analyses were implemented for gene, transposable element, and expression data analyses, and for comparative genomics such as ortholog predictions via a phylogenomic approach (GreenPhyl). Web tools have been developed or implemented to facilitate access to data, such as genetic makers (TropGeneDB), genetic maps (CMap), a physical Map (GBrowse), and Expressed sequence Tags (ESTtik) gene/TE predictions, and to allow online manual genome annotation (GnpAnnot). The number of tools may continue to grow, in particular with the near release of the Musa genome sequence, and the increase of Next-Generation Sequencing (NGS) facilities.
The GMGC website (http://www.musagenomics.org) is a place where data can be shared, and where databases and tools can be listed in an homogeneous way to serve the Musa genomics community. It is intended to provide the researchers interested in Musa with a common set of resources in order to work more efficiently and effectively.